



PCT10

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,594A

DATE: 07/16/2002

TIME: 14:58:14

Input Set : A:\5.1198 Sequence Listing.txt

Output Set: N:\CRF3\07162002\J088594A.raw

2 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
W--> 3 <120> TITLE OF INVENTION: Novel Transaldolase
W--> 4 <130> FILE REFERENCE: 00005.001198
W--> 5 <140> CURRENT APPLICATION NUMBER: US/10/088,594A
C--> 6 <141> CURRENT FILING DATE: 2002-06-11
7 <150> PRIOR APPLICATION NUMBER: JP 99/266548
8 <151> PRIOR FILING DATE: 1999-09-21
W--> 9 <160> NUMBER OF SEQ ID: 3
10 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1080
13 <212> TYPE: DNA
14 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
W--> 15 <400> SEQUENCE: 1

16	atg tct cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc	48
17	Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu	
18	1 5 10 15	
19	gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt	96
20	Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val	
21	20 25 30	
22	att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc	144
23	Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe	
24	35 40 45	
25	gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag	192
26	Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu	
27	50 55 60	
28	ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc	240
29	Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser	
30	65 70 75 80	
31	atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag	288
32	Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu	
33	85 90 95	
34	tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt	336
35	Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg	
36	100 105 110	
37	atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg	384
38	Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp	
39	115 120 125	
40	gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca	432

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41 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
42      130                      135                      140
43 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt      480
44 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
45 145                      150                      155                      160
46 aac gtc acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct      528
47 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
48      165                      170                      175
49 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta      576
50 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
51      180                      185                      190
52 tcc aag atc cac tct gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt      624
53 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
54      195                      200                      205
55 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct      672
56 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
57      210                      215                      220
58 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg      720
59 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
60 225                      230                      235                      240
61 tac aag gag ctt ttc gac gcc gcc gag ctg cct gaa ggt gcc aac act      768
62 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
63      245                      250                      255
64 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct      816
65 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
66      260                      265                      270
67 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc      864
68 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
69      275                      280                      285
70 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac      912
71 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
72      290                      295                      300
73 ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc      960
74 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
75 305                      310                      315                      320
76 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg      1008
77 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
78      325                      330                      335
79 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt      1056
80 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
81      340                      345                      350
E--> 82 gag tcc atg gaa gct cgc ctg aag
83 Glu Ser Met Glu Ala Arg Leu Lys
84      355                      360

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1080 ← insert nucleotide number at end of line

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108 <210> SEQ ID NO: 3
109 <211> LENGTH: 4108
110 <212> TYPE: DNA
111 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
112 <221> NAME/KEY: CDS → insert mandatory <220>

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113 <222> LOCATION: (373)..(2472)
W--> 114 <221> CDS Met Mandatey 2207
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118 ttgcaccgta ttgcttgccg aacatttttc ttttcctttc ggtttttcga gaattttcac 120
119 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacaccttt gacacatttg 180
120 aaccacagtt ggttataaaa tgggttcaac atcactatgg ttagagggtg tgacgggtca 240
121 gattaagcaa agactacttt cggggtagat cacctttgcc aaatttgaat caattaacct 300
122 aagtcgtaga tctgatcatc ggatctaacg aaaacgaacc aaaactttgg tcccggttta 360
123 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
124 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
125 1 5 10
126 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
127 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
128 15 20 25
129 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
130 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
131 30 35 40 45
132 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
133 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
134 50 55 60
135 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca 603
136 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
137 65 70 75
138 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag 651
139 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
140 80 85 90
141 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg 699
142 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
143 95 100 105
144 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac 747
145 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
146 110 115 120 125
147 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt 795
148 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
149 130 135 140
150 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc 843
151 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
152 145 150 155
153 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac 891
154 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
155 160 165 170
156 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct 939
157 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
158 175 180 185
159 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg 987
160 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
161 190 195 200 205

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162 ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct 1035
163 Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala
164 210 215 220
165 ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc 1083
166 Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr
167 225 230 235
168 att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg 1131
169 Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val
170 240 245 250
171 gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc 1179
172 Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg
173 255 260 265
174 acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg 1227
175 Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val
176 270 275 280 285
177 cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag 1275
178 His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu
179 290 295 300
180 ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc 1323
181 Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile
182 305 310 315
183 gct cac acc cgc tcc ctc gca gag cgc gct gca cag aag aag gct gca 1371
184 Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala
185 320 325 330
186 tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag 1419
187 Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys
188 335 340 345
189 gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct 1467
190 Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala
191 350 355 360 365
192 gac gag ctc cca aca tgg gat gca gat gag aag ggc gtc gca act cgt 1515
193 Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg
194 370 375 380
195 aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag 1563
196 Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu
197 385 390 395
198 ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc 1611
199 Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile
200 400 405 410
201 aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg 1659
202 Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp
203 415 420 425
204 tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac 1707
205 Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His
206 430 435 440 445
207 gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc 1755
208 Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg
209 450 455 460
210 cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca 1803

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211 Pro Tyr Gly Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala
212                               465                               470                               475
213 gtt cgt ctt gca gct ctc atg gag acc gac gct tac tac gtc tgg acc 1851
214 Val Arg Leu Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr
215                               480                               485                               490
216 cac gac tcc atc ggt ctg ggc gaa gat ggc cca acc cac cag cct gtt 1899
217 His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val
218                               495                               500                               505
219 gaa acc ttg gct gcg ctg cgc gcc atc cca ggt ctg tcc gtc ctg cgt 1947
220 Glu Thr Leu Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg
221 510                               515                               520                               525
222 cct gca gat gcg aat gag acc gcc cag gct tgg gct gca gca ctt gag 1995
223 Pro Ala Asp Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu
224                               530                               535                               540
225 tac aag gaa ggc cct aag ggt ctt gca ctg acc cgc cag aac gtt cct 2043
226 Tyr Lys Glu Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro
227                               545                               550                               555
228 gtt ctg gaa ggc acc aag gag aag gct gct gaa ggc gtt cgc cgc ggt 2091
229 Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly
230                               560                               565                               570
231 ggc tac gtc ctg gtt gag ggt tcc aag gaa acc cca gat gtg atc ctc 2139
232 Gly Tyr Val Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu
233                               575                               580                               585
234 atg ggc tcc ggc tcc gag gtt cag ctt gca gtt aac gct gcg aaa gct 2187
235 Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala
236 590                               595                               600                               605
237 ctg gaa gct gag ggc gtt gca gct cgc gtt gtt tca gtt cct tgc atg 2235
238 Leu Glu Ala Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met
239                               610                               615                               620
240 gat tgg ttc cag gag cag gac gca gag tac atc gag tcc gtt ctg cct 2283
241 Asp Trp Phe Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro
242                               625                               630                               635
243 gca gct gtg acc gct cgt gtg tct gtt gaa gct ggc atc gca atg cct 2331
244 Ala Ala Val Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro
245                               640                               645                               650
246 tgg tac cgc ttc ttg ggc acc cag ggc cgt gct gtc tcc ctt gag cac 2379
247 Trp Tyr Arg Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His
248                               655                               660                               665
249 ttc ggt gct tct gcg gat tac cag acc ctg ttt gag aag ttc ggc atc 2427
250 Phe Gly Ala Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile
251 670                               675                               680                               685
252 acc acc gat gca gtc gtg gca gcg gcc aag gac tcc att aac agt 2472
253 Thr Thr Asp Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Ser
254                               690                               695                               700
255 taattgccct gctgttttta gcttcaaccc ggggcagtat gattctccgg aattttattg 2532
256 ccccggttg ttgttgtaa tcggtacaaa gggctttaag cacatccctt acttgctgc 2592
257 tctccttgag cacagttcaa gaacaattct ttttaaggaaa atttagtttc atg tct 2648
258                               Met Ser

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W--> 259

1

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260	cac	att	gat	gat	ctt	gca	cag	ctc	ggc	act	tcc	act	tgg	ctc	gac	gac	2696
261	His	Ile	Asp	Asp	Leu	Ala	Gln	Leu	Gly	Thr	Ser	Thr	Trp	Leu	Asp	Asp	
262			5					10					15				
263	ctc	tcc	cgc	gag	cgc	att	act	tcc	ggc	aat	ctc	agc	cag	gtt	att	gag	2744
264	Leu	Ser	Arg	Glu	Arg	Ile	Thr	Ser	Gly	Asn	Leu	Ser	Gln	Val	Ile	Glu	
265		20					25					30					
266	gaa	aag	tct	gta	gtc	ggt	gtc	acc	acc	aac	cca	gct	att	ttc	gca	gca	2792
267	Glu	Lys	Ser	Val	Val	Gly	Val	Thr	Thr	Asn	Pro	Ala	Ile	Phe	Ala	Ala	
268	35					40					45					50	
269	gca	atg	tcc	aag	ggc	gat	tcc	tac	gac	gct	cag	atc	gca	gag	ctc	aag	2840
270	Ala	Met	Ser	Lys	Gly	Asp	Ser	Tyr	Asp	Ala	Gln	Ile	Ala	Glu	Leu	Lys	
271					55					60					65		
272	gcc	gct	ggc	gca	tct	gtt	gac	cag	gct	gtt	tac	gcc	atg	agc	atc	gac	2888
273	Ala	Ala	Gly	Ala	Ser	Val	Asp	Gln	Ala	Val	Tyr	Ala	Met	Ser	Ile	Asp	
274				70				75						80			
275	gat	gtt	cgc	aat	gct	tgt	gat	ctg	ttc	acc	ggc	atc	ttc	gag	tcc	tcc	2936
276	Asp	Val	Arg	Asn	Ala	Cys	Asp	Leu	Phe	Thr	Gly	Ile	Phe	Glu	Ser	Ser	
277			85					90					95				
278	aac	ggc	tac	gac	ggc	cgc	gtg	tcc	atc	gag	gtt	gac	cca	cgt	atc	tct	2984
279	Asn	Gly	Tyr	Asp	Gly	Arg	Val	Ser	Ile	Glu	Val	Asp	Pro	Arg	Ile	Ser	
280		100					105					110					
281	gct	gac	cgc	gac	gca	acc	ctg	gct	cag	gcc	aag	gag	ctg	tgg	gca	aag	3032
282	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Ala	Gln	Ala	Lys	Glu	Leu	Trp	Ala	Lys	
283	115					120					125					130	
284	gtt	gat	cgt	cca	aac	gtc	atg	atc	aag	atc	cct	gca	acc	cca	ggt	tct	3080
285	Val	Asp	Arg	Pro	Asn	Val	Met	Ile	Lys	Ile	Pro	Ala	Thr	Pro	Gly	Ser	
286				135						140					145		
287	ttg	cca	gca	atc	acc	gac	gct	ttg	gct	gag	ggc	atc	agc	gtt	aac	gtc	3128
288	Leu	Pro	Ala	Ile	Thr	Asp	Ala	Leu	Ala	Glu	Gly	Ile	Ser	Val	Asn	Val	
289				150					155					160			
290	acc	ttg	atc	ttc	tcc	gtt	gct	cgc	tac	cgc	gag	gtc	atc	gct	gcg	tac	3176
291	Thr	Leu	Ile	Phe	Ser	Val	Ala	Arg	Tyr	Arg	Glu	Val	Ile	Ala	Ala	Tyr	
292			165					170					175				
293	atc	gag	gga	atc	aag	cag	gca	gct	gca	aac	ggc	cac	gac	gta	tcc	aag	3224
294	Ile	Glu	Gly	Ile	Lys	Gln	Ala	Ala	Ala	Asn	Gly	His	Asp	Val	Ser	Lys	
295		180					185				190						
296	atc	cac	tct	gtg	gct	tcc	ttc	ttc	gtc	tcc	cgc						

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309	Pro	Leu	Trp	Ala	Ser	Thr.	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala	Ala	Thr	
310		260					265					270					
311	ctt	tac	gtt	tcc	gag	ctg	gct	ggc	cca	aac	acc	gtc	aac	acc	atg	cca	3512
312	Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr	Met	Pro	
313	275					280					285					290	
314	gaa	ggc	acc	atc	gac	gct	gtt	ctg	gaa	ctg	ggc	aac	ctg	cac	ggc	gac	3560
315	Glu	Gly	Thr	Ile	Asp	Ala	Val	Leu	Glu	Leu	Gly	Asn	Leu	His	Gly	Asp	
316					295					300					305		
317	acc	ctg	tcc	aac	tcc	gcg	gca	gaa	gct	gac	gct	gtg	ttc	tcc	cag	ctt	3608
318	Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser	Gln	Leu	
319				310					315					320			
320	gag	gct	ctg	ggc	gtt	gac	ttg	gca	gat	gtc	ttc	cag	gtc	ctg	gag	acc	3656
321	Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu	Glu	Thr	
322			325					330					335				
323	gag	ggc	gtg	gac	aag	ttt	gtt	gct	tct	tgg	agc	gaa	ctg	ctt	gag	tcc	3704
324	Glu	Gly	Val	Asp	Lys	Phe	Val	Ala	Ser	Trp	Ser	Glu	Leu	Leu	Glu	Ser	
325		340					345					350					
326	atg	gaa	gct	cgc	ctg	aag	tagaatcagc	acgctgcac	agtaacggcg								3752
327	Met	Glu	Ala	Arg	Leu	Lys											
328	355					360											
329	acatgaaaac		gaattagttc			gatcttatgt		ggccggttac		catctttcat		taaagaaagg					3812
330	atcgtgacgc		taccatcgtg			agcacacaac		cgacccccctc		cagctggaca		aacctactgc					3872
331	gcgacccgca		ggataaacga			ctcccocgca		tcgctggccc		ttccggcatg		gtgatcttcg					3932
332	gtgtcactgc		cgacttggtc			cgaagggaagc		tgctccccgc		catttatgat		ctagcaaacc					3992
333	gcggattgct		gcccccagga			ttctcgttgg		taggttaacg		ccgcgcgaa		tggtccaaag					4052
334	aaqactttga		aaaatacgta			cgcgatgccg		caagtgcctg		tgctcgtaag		gaattc					4108

VERIFICATION SUMMARY

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TIME: 14:58:15

Input Set : A:\5.1198 Sequence Listing.txt

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L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:1
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:116 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3